



IFWO

RAW SEQUENCE LISTING

DATE: 10/12/2004

PATENT APPLICATION: US/10/763,976A

TIME: 12:30:42

Input Set : D:\Warf Sequence.ST25.txt

Output Set: N:\CRF4\10122004\J763976A.raw

3 <110> APPLICANT: Harms, Jerome S
 4 Splitter, Gary A
 5 Eakle, Kurt A
 6 Bremel, Robert D
 8 <120> TITLE OF INVENTION: Inducible Protein Expression System
 10 <130> FILE REFERENCE: 2240/3
 12 <140> CURRENT APPLICATION NUMBER: US 10/763,976A
 13 <141> CURRENT FILING DATE: 2004-01-23
 15 <160> NUMBER OF SEQ ID NOS: 65
 17 <170> SOFTWARE: PatentIn version 3.3
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 576
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Artificial
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: Engineered Sequence from virus and plasmid
 28 <220> FEATURE:
 29 <221> NAME/KEY: Promoter
 30 <222> LOCATION: (87)..(432)
 31 <223> OTHER INFORMATION: BLV Promoter
 33 <400> SEQUENCE: 1
 34 aggaaaccag cagcggctat ccgcgcacatcc atgcccccca actgcaggag tggggaggga 60
 36 cgatggccgc tttggtcgag gcggatccta gcagaaaaat aagacttgat tcccccttaa 120
 38 aattacaact gctagaaaat gaatggctct cccgcctttt ttgaggggga atcatttgta 180
 40 tgaaagatca tgccgaccta ggcgcgcgcca ccgccccgta aaccagacag agacgtcagc 240
 42 tgccagaaaa gctggtgacg gcagctgggtg gctagaatcc ccgtacctcc ccaacttccc 300
 44 ctttcccgaa aaatccacac cctgagctgc tgacctcacc tgctgataaa ttaataaaat 360
 46 gccggccctg tgcagtttagc ggcaccagaa gcgttcttct cctgagaccc tcgtgctcag 420
 48 ctctcggtcc tgcctcgaga agcttggttat cacaagtttg tacaaaaaag ctgaacgaga 480
 50 aacgtaaaat gatataaata tcaatatatt aaattagatt ttgcataaaa aacagactac 540
 52 ataatactgt aaaacacaac atatccagtc actatg 576
 55 <210> SEQ ID NO: 2
 56 <211> LENGTH: 930
 57 <212> TYPE: DNA
 58 <213> ORGANISM: Bovine leukemia virus
 61 <220> FEATURE:
 62 <221> NAME/KEY: CDS
 63 <222> LOCATION: (1)..(930)
 65 <400> SEQUENCE: 2
 66 atg gca agt gtt gtt ggt tgg ggg ccc cac tct cta cat gcc tgc ccg 48
 67 Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
 68 1 5 10 15
 70 gcc ctg gtt ttg tcc aat gac gtc acc atc gat gcc tgg tgc ccc ctc 96



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71 Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
72          20          25          30
74 tgc ggg ccc cat gag cga ctc caa ttc gaa agg atc gac acc acg cac      144
75 Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr His
76          35          40          45
78 acc tgc gag acc cac cgt atc acc tgg acc gcc gat gga cga cct ttc      192
79 Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp Gly Arg Pro Phe
80          50          55          60
82 ggc ctc aat gga gcg ctg ttc cct cga ctg cat gtc tcc aga gac ccg      240
83 Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His Val Ser Arg Asp Pro
84 65          70          75          80
86 gcc cca agg gcc cga cga ctc tgg atc aac tgc ccc ctt ccg gcc gtt      288
87 Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
88          85          90          95
90 cgc gct cag ccc ggc ccg gtt tca ctt tcc ccc ttc gag cgg tcc ccc      336
91 Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
92          100          105          110
94 ttc cag ccc tac caa tgc caa ttg ccc tcg gcc tct agc gac ggt tgc      384
95 Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
96          115          120          125
98 ccc gtc atc ggg cac ggc ctt ctt ccc tgg aac aac tta gta acg cat      432
99 Pro Val Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
100          130          135          140
102 cct tgt cct cgg aaa gtc ctt ata tta aat caa atg gcc aat ttt tcc      480
103 Pro Cys Pro Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
104 145          150          155          160
106 tta ctc ccc ccc ttc aat acc ctc ctt gtg gac ccc ctc cgg ttg tcc      528
107 Leu Leu Pro Pro Phe Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
108          165          170          175
110 gtc ttt gcc cca gac acc agg gga gcc ata cgt tat ctc tcc acc ctt      576
111 Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
112          180          185          190
114 ttg acg cta tgc cca gct act tgt att cta ccc ctc ggc gag ccc ttc      624
115 Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
116          195          200          205
118 tct cct aat gtc ccc ata tgt cgc ttt ccc cgg gac tcc aat gaa ccc      672
119 Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
120          210          215          220
122 ccc ctt tca gaa ttc gag ctg ccc ctt atc caa acg ccc ggc ctg tct      720
123 Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
124 225          230          235          240
126 tgg tct gtc ccc gcg atc gac cta ttc cta acc ggc ccc cct tcc cca      768
127 Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
128          245          250          255
130 tgc gac cgg tta cac gta tgg tcc agt cct cag gcc tta cag cgc ttc      816
131 Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
132          260          265          270
134 ctc cat gac cct acg cta acc tgg tca gaa ttg gtt gct agc agg aaa      864
135 Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys

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136          275          280          285
138 cta aga ctt gat tca ccc tta aaa tta caa ctg tta gaa aat gaa tgg      912
139 Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
140          290          295          300
142 ctc tcc cgc ctt ttt tga      930
143 Leu Ser Arg Leu Phe
144 305
147 <210> SEQ ID NO: 3
148 <211> LENGTH: 309
149 <212> TYPE: PRT
150 <213> ORGANISM: Bovine leukemia virus
152 <400> SEQUENCE: 3
154 Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
155 1          5          10          15
158 Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
159          20          25          30
162 Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr His
163          35          40          45
166 Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp Gly Arg Pro Phe
167          50          55          60
170 Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His Val Ser Arg Asp Pro
171 65          70          75          80
174 Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
175          85          90          95
178 Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
179          100          105          110
182 Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
183          115          120          125
186 Pro Val Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
187          130          135          140
190 Pro Cys Pro Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
191 145          150          155          160
194 Leu Leu Pro Pro Phe Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
195          165          170          175
198 Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
199          180          185          190
202 Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
203          195          200          205
206 Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
207          210          215          220
210 Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
211 225          230          235          240
214 Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
215          245          250          255
218 Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
219          260          265          270
222 Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
223          275          280          285
226 Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp

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227      290      295      300
230 Leu Ser Arg Leu Phe
231 305
234 <210> SEQ ID NO: 4
235 <211> LENGTH: 1062
236 <212> TYPE: DNA
237 <213> ORGANISM: Human T-cell lymphotropic virus type 1
240 <220> FEATURE:
241 <221> NAME/KEY: promoter
242 <222> LOCATION: (1)..(353)
244 <400> SEQUENCE: 4
245 atggcccact tcccagggtt tggacagagt cttcttttcg gatacccagt ctacgtgttt      60
247 ggagacggcg actggtgccc ctgtgtacaa atctctgggg gactatgttc ggcccgccta      120
249 catcgtcacg cctactggc cactgtcca gagcatcaga tcacctggga ccccatcgat      180
251 ggacgcgtta tcggtcagc tctacagttc cttatccctc gactccctc cttccccacc      240
253 cagagaacct ctaagacct caaggtcctt acccgcgcaa tcatcatac aacccccaac      300
255 attccaccct ccttcctcca ggccatgctc aaatactccc cttccgaaa tggatacatg      360
257 gaaccacccc ttgggcagca cctcccaacc ctgtcttttc cagaccccg actccggccc      420
259 caaacctgt acaccctctg gggaggctcc gttgtctgca tgtacctcta ccagctttcc      480
261 ccccccatca cctggcccct cctgcccac gtgattttt gccaccccg ccagctcggg      540
263 gccttctca ccaatgttcc ctacaagcga atagaagaac tcctctataa aatttcctt      600
265 accacagggg ccctaataat tctaccgaa gactgtttgc ccaccacct tttccagcct      660
267 gttagggcac ccgtcacgct aacagcctgg caaacggcc tccttcggt ccaactcaacc      720
269 ctcaccactc caggccttat ttggacattt accgatggca cgcctatgat ttccggggccc      780
271 tgccctaaag atggccagcc atctttagta ctacagtcct cctcctttat atttcacaaa      840
273 tttcaaacca aggcctacca cccctcattt ctactctcac acggcctcat acagtactct      900
275 tcctttcata atttacatct cctgtttgaa gaatacacca acatccccat ttctctactt      960
277 ttttaaaaaa aagaggcaga tgacaatgac catgagcccc aaatatcccc cgggggctta      1020
279 gagcctccca gtgaaaaaca tttccgcgaa acagaagtct ga      1062
282 <210> SEQ ID NO: 5
283 <211> LENGTH: 353
284 <212> TYPE: DNA
285 <213> ORGANISM: Human T-cell lymphotropic virus type 1
287 <400> SEQUENCE: 5
288 tgacaatgac catgagcccc aaatatcccc cgggggctta gagcctctca gtgaaaaaca      60
290 tttccgtgaa acagaagtct gagaagggtc gggcccagaa taaggctctg acgtctcccc      120
292 ccggaggaca gctcagcacc agctcaggct aggcctgac gtgtccccct aaagacaaat      180
294 cataagctca gacctccggg aagccaccgg gaaccaccca tttcctcccc atgtttgtca      240
296 agccgtcctc aggcgttgac gacaaccct cactcaaaa aacttttcat ggcacgcata      300
298 cggctcaata aaataacagg agtctataaa agcgtgggga cagttcagga ggg      353
301 <210> SEQ ID NO: 6
302 <211> LENGTH: 456
303 <212> TYPE: DNA
304 <213> ORGANISM: Human immunodeficiency virus type 1
307 <220> FEATURE:
308 <221> NAME/KEY: CDS
309 <222> LOCATION: (1)..(456)
311 <400> SEQUENCE: 6
312 ctg gaa ggg cta att tgg tcc caa aga aga caa gag atc ctt gat ctg      48

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Input Set : D:\Warf Sequence.ST25.txt

Output Set: N:\CRF4\10122004\J763976A.raw

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313 Leu Glu Gly Leu Ile Trp Ser Gln Arg Arg Gln Glu Ile Leu Asp Leu
314 1          5          10          15
316 tgg atc tac cac aca caa ggc tac ttc cct gat tgg cag aat tac aca      96
317 Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
318          20          25          30
320 cca ggg cca ggg atc aga tat cca ctg acc ttt gga tgg tgc ttc aag      144
321 Pro Gly Pro Gly Ile Arg Tyr Pro Leu Thr Phe Gly Trp Cys Phe Lys
322          35          40          45
324 cta gta cca gtt gag cca gag aag gta gaa gag gcc aat gaa gga gag      192
325 Leu Val Pro Val Glu Pro Glu Lys Val Glu Glu Ala Asn Glu Gly Glu
326          50          55          60
328 aac aac agc ttg tta cac cct atg agc ctg cat ggg atg gag gac gcg      240
329 Asn Asn Ser Leu Leu His Pro Met Ser Leu His Gly Met Glu Asp Ala
330 65          70          75          80
332 gag aaa gaa gtg tta cac cct atg agc ctg cat ggg atg gag gac gcg      288
333 Glu Lys Glu Val Leu Val Trp Arg Phe Asp Ser Lys Leu Ala Phe His
334          85          90          95
336 cac atg gcc cga gag ctg cat ccg gag tac tac aaa gac tgc tga cat      336
337 His Met Ala Arg Glu Leu His Pro Glu Tyr Tyr Lys Asp Cys His
338          100          105          110
340 cga gct ttc tac aag gga ctt tcc gct ggg gac ttt cca ggg agg cgt      384
341 Arg Ala Phe Tyr Lys Gly Leu Ser Ala Gly Asp Phe Pro Gly Arg Arg
342          115          120          125
344 ggc ctg ggc ggg act ggg gag tgg cgt ccc tca gat gct gca tat aag      432
345 Gly Leu Gly Gly Thr Gly Glu Trp Arg Pro Ser Asp Ala Ala Tyr Lys
346          130          135          140
348 cag ctg ctt ttt gcc tgt act ggg      456
349 Gln Leu Leu Phe Ala Cys Thr Gly
350          145          150
353 <210> SEQ ID NO: 7
354 <211> LENGTH: 110
355 <212> TYPE: PRT
356 <213> ORGANISM: Human immunodeficiency virus type 1
358 <400> SEQUENCE: 7
360 Leu Glu Gly Leu Ile Trp Ser Gln Arg Arg Gln Glu Ile Leu Asp Leu
361 1          5          10          15
364 Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
365          20          25          30
368 Pro Gly Pro Gly Ile Arg Tyr Pro Leu Thr Phe Gly Trp Cys Phe Lys
369          35          40          45
372 Leu Val Pro Val Glu Pro Glu Lys Val Glu Glu Ala Asn Glu Gly Glu
373          50          55          60
376 Asn Asn Ser Leu Leu His Pro Met Ser Leu His Gly Met Glu Asp Ala
377 65          70          75          80
380 Glu Lys Glu Val Leu Val Trp Arg Phe Asp Ser Lys Leu Ala Phe His
381          85          90          95
384 His Met Ala Arg Glu Leu His Pro Glu Tyr Tyr Lys Asp Cys
385          100          105          110
388 <210> SEQ ID NO: 8

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/12/2004
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

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Seq#:38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61
Seq#:62,63,64,65

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/763,976A

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Input Set : D:\Warf Sequence.ST25.txt

Output Set: N:\CRF4\10122004\J763976A.raw